

Role of social wasps in *Saccharomyces cerevisiae* ecology and evolution

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Saccharomyces cerevisiae is one of the most important model organisms and has been a valuable asset to human civilization. However, despite its extensive use in the last 9,000 y, the existence of a seasonal cycle outside human-made environments has not yet been described. We demonstrate the role of social wasps as vector and natural reservoir of *S. cerevisiae* during all seasons. We provide experimental evidence that queens of social wasps overwintering as adults (*Vespa crabro* and *Polistes* spp.) can harbor yeast cells from autumn to spring and transmit them to their progeny. This result is mirrored by field surveys of the genetic variability of natural strains of yeast. Microsatellites and sequences of a selected set of loci able to recapitulate the yeast strain's evolutionary history were used to compare 17 environmental wasp isolates with a collection of strains from grapes from the same region and more than 230 strains representing worldwide yeast variation. The wasp isolates fall into subclusters representing the overall ecological and industrial yeast diversity of their geographic origin. Our findings indicate that wasps are a key environmental niche for the evolution of natural *S. cerevisiae* populations, the dispersion of yeast cells in the environment, and the maintenance of their diversity. The close relatedness of several wasp isolates with grape and wine isolates reflects the crucial role of human activities on yeast population structure, through clonal expansion and selection of specific strains during the bio-transformation of fermented foods, followed by dispersal mediated by insects and other animals.

evolutionary biology | genomics

The yeast *Saccharomyces cerevisiae* is one of the microorganisms most appreciated by humans because of its utility in the production of food and drink. The discovery of ancient *S. cerevisiae* DNA in Chinese pots (7,000–5,500 BC) (1) and in jars of the King Scorpion tomb in Abydos (3,150 B.C.) (2) have allowed us to date the first observed wine fermentations back to proto-historic periods. Although we have thorough knowledge regarding the genetic, molecular, and phenotypic traits arising from the wide use of *S. cerevisiae*, its origin and evolution are still debated. Some scientists hypothesize that this organism evolved in human-associated environments, where selective pressure (such as high ethanol concentrations in must fermentation) allowed yeast speciation (3). The recent finding of *S. cerevisiae* DNA in Miocene and Oligocene ambers indicates that the budding yeast existed long before human advent (4). The discussion on domestication then moved from the species level to the strain level, with genetic evidence suggesting that strains used for fermentation have been selected and domesticated from wild strains, and then dispersed (5). However, it is still unclear how *S. cerevisiae* cells spread among different environments. Polsinelli et al. reported that, before maturation, grapes are almost free of *S. cerevisiae* (~0.05%), whereas 25% of ripe damaged grapes harbor such cells (6, 7). Following this pioneering study, *S. cerevisiae* strains have been isolated from several natural sources

(7–22). However, these reports are restricted to warm seasons, when ripe fruit is available, or to post harvest. Even if a natural origin of *S. cerevisiae* is no longer under debate, the crucial question regarding its ecological sanctuaries in the absence of sugar-rich fruits and far from protected human environments remains to be explained. Answering this question might furnish fundamental information regarding its evolution. It must be noted that *S. cerevisiae* is not airborne, but requires a vector to move (23). Several studies show a flow of *S. cerevisiae* cells among wineries and natural environments (24), probably favored by animal vectors (25). In a recent paper, Francesca et al. suggest the role of migratory birds as vectors of *S. cerevisiae* cells (26). Nevertheless, no indications of the periods of yeast isolation were given. Moreover, these authors showed that yeast cells persisted in the bird's gut for no longer than 12 h, indicating that birds cannot act as environmental reservoirs for this microorganism. It has been reported that yeasts are associated with insects (23, 27–29) during grape harvest season. Stevic et al. (30) showed that bees and wasps act as carriers of yeasts in autumn and that honey bee hives contain yeasts during the winter. Unfortunately, in these reports no details were provided about the presence of *S. cerevisiae* within the identified yeast species. Social wasps are very promising as potential yeast vectors. Their colony cycle initiates in spring when new nests are founded by females emerging in the previous autumn that overwintered after being fertilized. These foundresses feed the larvae with regurgitated food (trophallaxis), allowing a possible transgenerational passage of yeasts, which could be continued by food exchange between overlapping generations of workers and future foundresses as well. Moreover, the number of adult wasps in a given locality presents a significant peak in concomitance with grape maturation, and wasps are well known to feed on this fruit (*SI Appendix, Fig. S1*). In particular, *Vespa crabro* wasps, which are common in Mediterranean and Southern European countries, have a buccal apparatus that allows them to break hard substrates, such as the skin of pristine grapes. Social wasps comprise a very large niche including most of the environments where yeasts can be found. Adults feed mainly on sugar sources, need wood fibers to construct their nests,

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different clusters. Ten wasp isolates were related to wine strains, three to a group of strains found in bread, one to a mixed group encompassing African beer, palm wine isolates and laboratory strains, and one to a group containing natural isolates found in African palm wines. Some wasp strains (F31x, Buc1, E32, and NPSM) sampled in different periods of the year contained almost identical genotypes, forming a subgroup within a larger cluster containing many wine and grape strains from Tuscany, a starter strain (Lallemand 6009) and three Italian clinical isolates (YJM975, YJM978, and YJM981). The Sgv114 wasp isolate clustered in a subgroup composed of almost only sympatric strains, two from wine (SG10 and SG60) and three from grapes (SGU165, SGU89, SGU25) (Fig. 2, IV) isolated from the same vineyard in the same year. As expected, several strains isolated from insects collected the same day in the same location show a strong genetic similarity (BIBVC4.3 and BIBVC5.3, collected near Florence, and YVC1E2, YVC2E6, and YVC4EST1, isolated from insects caught on Elba island) (Fig. 2, II and V). At the same time, strain BIBVC1.1, collected before grape maturation, and its sympatric BIBVC strains, show high genetic divergence, being the first strain strictly similar to the YVCE4 strain. BIBVC1.1 and YVCE4 strains were isolated from insects caught before grape maturation in different sites distant ~40 km from each other. Similarly, the BIBVC4.3 and BIBVC5.3 strains are highly similar to the YVPC7.6 strain, isolated from different insect species (*V. crabro* the first two, *P. dominula* the third) in locations almost 20 km apart.

The structure of a population composed of subgroups can be described by identifying the most probable ancestor for each group, namely an individual from which all of the organisms in the subgroup are directly descended. To support the global structure

observed from microsatellite typing, we used a Bayesian algorithm to infer the most probable partition of the 256 strains into 13 groups or ancestral lineages (Fig. 2B). Wine strains were placed into five main groups. Tuscan grape strains were inferred to descend from the same ancestors as the Tuscan wine strains and from a fourth European ancestor, not shared with the Tuscan wine group (bright blue in Fig. 2B). This result indicates the presence of a specific yeast “microbiota” in geographically and climatically different regions having a millenary culture of production of fermented food and drink. Strains isolated from humans and other animals did not have a specific ancestor, but rather the vast majority of ancestors belonging to different groups. Wasp isolates were placed into four main groups, two of which were shared with European wine isolates, one an ancestor of bread isolates and the fourth typical of laboratory strains. Laboratory strains have a natural origin (i.e., rotten figs, soil) whose ancestor is also shared with US oak, palm wine, and clinical strains.

In addition to microsatellite analysis, we assessed strain relatedness by using three gene sequences recently shown to recapitulate the genetic relatedness and population structure that could be obtained by means of entire genome sequencing (34). The cluster obtained describes an overall scenario similar to that observed with microsatellite analysis (Fig. 3). Indeed, the Mantel test performed on the distance matrices obtained by microsatellites and gene sequence analyses showed a highly significant correlation ($P < 0.001$). Nevertheless, many strain pairs showing high distances in microsatellites have low dissimilarity in the three genes, thus resulting in a relatively low Pearson R (0.340) (SI Appendix, Fig. S5). This is expected in the case of mosaic genomes. When repeating the clustering using strains of *S. paradoxus* (the closest known relative of *S. cerevisiae*) as root (SI

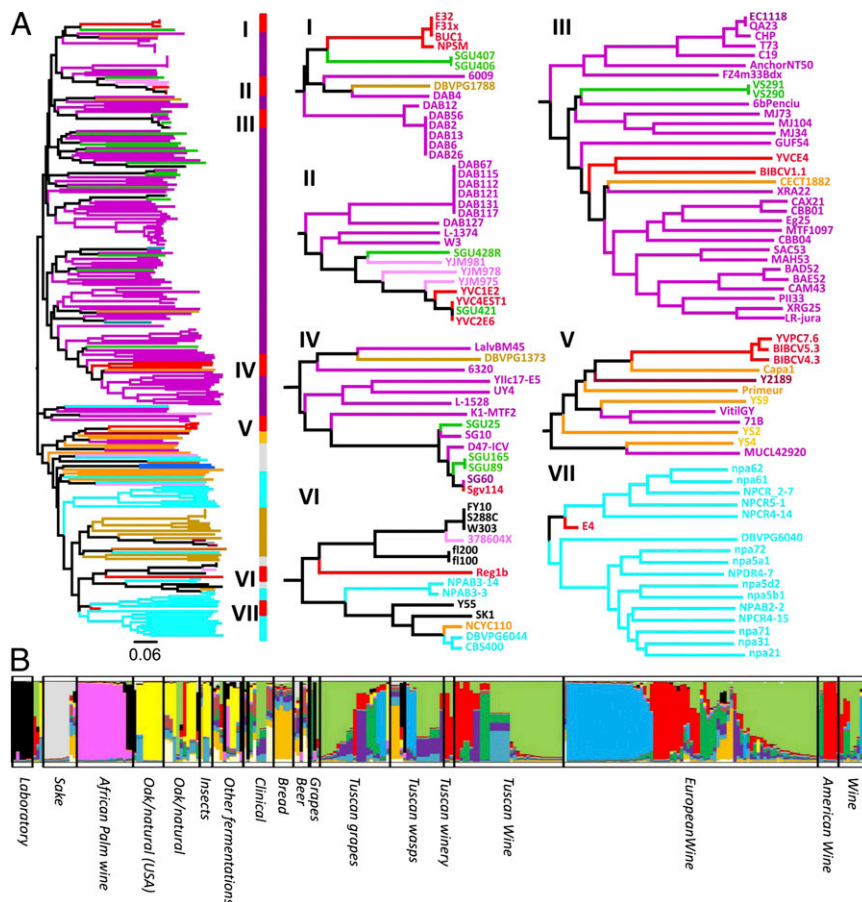
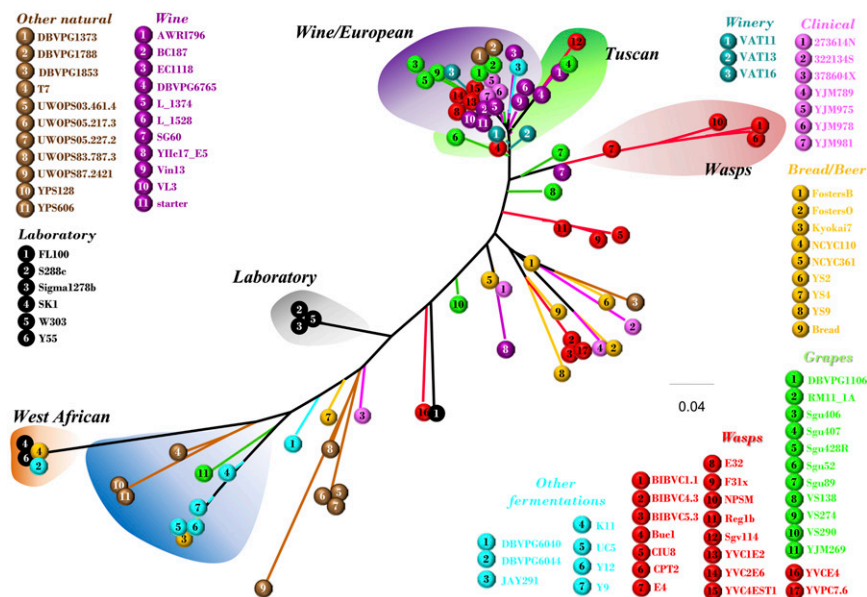


Fig. 2. Microsatellite analysis results. (A) Neighbor-joining tree showing the clustering of 17 *S. cerevisiae* wasp isolates among 256 yeast strains obtained from different sources. The tree was constructed from the Chord distance between strains based on the polymorphism at 12 loci and was rooted according to the midpoint method. Branches are colored according to the substrate from which strains have been isolated. Color code: red, insect isolates; purple, wine; green, grapes; orange, baked products and beer; pink, clinical; light blue, other fermentations; light brown, other natural sources. The position of wasp isolates within the tree is indicated by a red bar. I, II, III, IV, V, VI, and VII: detail of the subclusters encompassing wasp isolates. (B) Ancestry of the 256 *S. cerevisiae* strains analyzed by microsatellite analysis. The figure shows the proportion of each strain's ancestry in each cluster. This set of strains as a whole was inferred to fall into 13 clusters. Vertical lines are partitioned into 13 colored components (each representing one of the most probable inferred ancestors, or K clusters), which represent the individual's estimated membership coefficients in the K clusters. Ancestry was inferred by Instruct analysis (53) and drawn with Distruct (54).



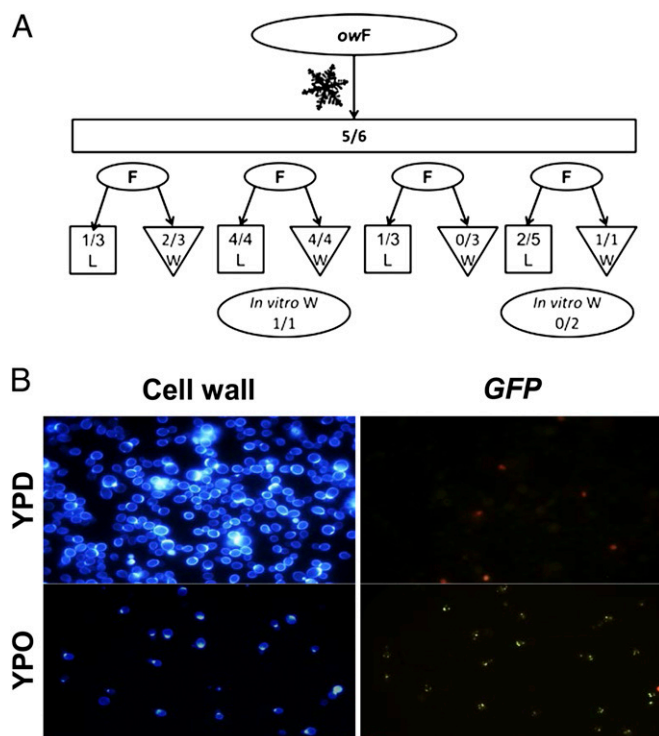


Fig. 4. *Polistes* spp. insects fed with *S. cerevisiae* cells can maintain the yeast in their gut during the winter and pass them to their progeny after nest foundation in the spring. (A) Five out of six overwintering wasps fed with the labeled yeast strain BY4742-GFP/FOX3 preserved the yeast throughout the winter. Four of four foundresses allowed to form a colony were able to spread yeast cells to their offspring both at the larval stage and after their emergence. F = foundress; in vitro W = worker emerged in vitro; L = larva; owF = overwintering foundress; W = worker. (B) Visualization of BY4742-GFP/FOX3 cells in several conditions (original magnification, 100 \times). Yeast cell wall was visualized with Calcofluor white (blue). Green fluorescence is only produced by the tagged strain when grown in YPO medium (Yeast Peptone 0.2% Oleate medium). Red auto-fluorescence is due to intracellular NADH accumulation in necrotic cells (55).

because wasps can harbor ingested yeast cells for a short time, as it occurs for birds, and continuously renew their microflora by trophic events. However, we experimentally demonstrated that hibernating female foundresses can harbor yeast cells from autumn to spring and then pass them to the next generation in a theoretically unending transmission phenomenon. The role of wasps in maintaining yeast cells during the winter and disseminating them before, during and after the grape harvest, fills the gap left by previous findings indicating a yeast flow between the winery and the vineyard (24, 40–42) but which failed to explain the annual persistence of yeast strains in the soil or in grapes (43).

The use of two different markers, microsatellites and genome-mimicking genes, permits estimation of the genetic evolution of yeast strains at different levels. Both microsatellite and sequence analyses revealed that *S. cerevisiae* did not evolve specific strains associated with animals. Conversely, the genome complexity borne by yeast wasp isolates revealed ancestors common to wine, grapes, bread, and oak yeast isolates. This suggests that yeasts are not subject to strong constraints when in association with animals and that there exists a continuous exchange of cells from animals to different sources and vice versa. The great genetic distance observed between some wasp strains and those isolated from grapes from the same area and a nearby winery strengthens the hypothesis about a multidirectional flow of *S. cerevisiae* occurring not only between wineries and vineyards, but among different sources as well.

Our findings provide a unique illustration of the entire natural cycle of *S. cerevisiae* in at least one ecological environment the gut of social wasps—that, in association with a series of other human and wild environments, significantly contributes to complete the niche, population structure, and diversity of yeast. Wasps can maintain a potentially unending transmission of yeast strains through favorable and unfavorable seasons and also function as vectors to suitable targets (ripe fruits) in suitable seasons (the end of summer). We do not claim that the social wasp gut is the only niche where *S. cerevisiae* is able to survive throughout the year, but we propose that hibernating social wasps have a preferential role in disseminating yeasts compared with other insects.

Our results also reveal that yeast strains in wasps, grapes, and fermentation from the same vineyard, even in different months and years, are more similar than strains deriving from other environmental and geographical locations. In this perspective, wasps could play a role both in maintaining ecological diversity and in conserving the yeast populations evolved in human “ersatz” environments established throughout the centuries by means of vine culture and wine production. The conservation of such diversity may have potential industrial importance in preserving the quality of typical fermented products. This suggests that any environmental change affecting insect biodiversity may create a substantial risk of reducing yeast biodiversity and consequently have an impact on the quality of fermented products.

Methods

Insect Collection and Dissection, and Yeast Isolation and Identification. Adult wasps and bees were dissected in sterile Petri dishes using sterile clamps under a stereomicroscope. Intestines were extracted and their content suspended in sterile water. The obtained solution was plated on YPD supplemented with penicillin and streptomycin (44). The identification of the isolated yeast strains was carried out by sequencing the ribosomal intergenic region as described by Sebastiani et al. (45). Associations between the presence of different yeast species and the collection period in each examined insect gut have been assessed by correspondence analysis by using the *ade4* R package (46).

Sequencing DNA of *S. cerevisiae* Strains. Three genes, *URN1*, *EXO5* and *IRC8*, able to recapitulate the entire genome (34), have been sequenced. Primers used for both amplifications and sequencing are listed in *SI Appendix, Table S3*. Sequences (analyzed samples are listed in *SI Appendix, Table S2*) were compared with *S. cerevisiae* pre-identified sequences downloaded from the Sanger institute (35) and from the SGD (47) websites. Phylogenetic analysis and tree drawing were carried out as described by Ramazzotti et al. (34). Populations were inferred using *Structure* (48) and *dapc* (differential analysis of principal components) in *SI Appendix*. The results of 10 independent *Structure* chains were combined with CLUMPP (49). These sequence data have been deposited in the GenBank database under accession nos. JQ946429–JQ946518.

Microsatellite Characterization. A set of 256 *Saccharomyces cerevisiae* strains, listed in *SI Appendix, Table S4*, was characterized for allelic variation at 12 microsatellites (50). The chord distance *D_c* matrix (51) was calculated. The tree was obtained from the distance matrices with Neighbor of the Phylip 3.67 package, and drawn using MEGA5.05 (52). The tree was rooted by the midpoint method. To assess the assignment of each insect yeast strain to a specific origin, Instruct (53) was used to evaluate the number of populations that can be observed in this set of strains. The results of 10 independent chains were combined with CLUMPP (49), and the consensus file was illustrated with Distruct (54).

Overwintering Wasps. In November, at the beginning of the hibernation, 20 *Polistes* spp. wasps were fed 10^8 cells of BY4742-GFP/FOX3 (Mat α *his3 Δ 1 leu2 Δ 0 lys2 Δ 0 ura3 Δ 0*). *S. cerevisiae* isolates were identified by sequencing the ribosomal intergenic region as described by Sebastiani et al. (45). *S. cerevisiae* isolates were then grown in rich medium supplemented with 0.2% oleate. BY4742-GFP/FOX3 isolates were identified with fluorescence microscopy able to express the GFP-labeled Fox3 protein. FOX3 gene expression is positively regulated by the presence of oleate as a carbon source. The strain used herein is able to express a Fox3p labeled with green at the

peroxisomal level, as shown in Fig. 4B. Fed wasps were allowed to hibernate. At the end of the hibernation, some wasps were dissected and the contents of their guts were treated as previously described.

Colony-Founding Wasps. Four colonies of *Polistes dominula* were collected at the pre-emerging phase before worker emergence. At that stage, colonies were composed of the adult foundresses and by larvae and pupae of their first daughters. We fed each foundress 10^8 cells of the BY4742-GFP/FOX3 strain. During the following 10 d, a number of workers emerged having then adult–adult trophic interactions. Some *Polistes* pupae were removed from nests before their emergence. Such pupae were allowed to emerge in clean

tubes to avoid any adult–adult contact. Larvae, worker wasps emerging in the colony, and worker wasps emerging without contact with the adults were dissected, and the contents of their guts were treated as previously described.

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